



## An Integrated Genomics Framework for System-Level Cell Factory Design

Cardinale, Stefano; Ye, Lumeng; Sommer, Morten Otto Alexander

*Publication date:*  
2016

*Document Version*  
Publisher's PDF, also known as Version of record

[Link back to DTU Orbit](#)

*Citation (APA):*  
Cardinale, S., Ye, L., & Sommer, M. O. A. (2016). *An Integrated Genomics Framework for System-Level Cell Factory Design*. Abstract from An Integrated Genomics Framework for System-Level Cell Factory Design , Milano, Italy.

---

### General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

## **Abstract**

### **Title: An Integrated Genomics Framework for System-Level Cell Factory Design**

Cardinale S., Ye L., Sommer M.

We combine barcoded mutagenesis and molecular biosensors to study the genetic and metabolic adaptation to the overexpression of enzymes for regenerating fundamental cellular biosynthetic precursors and co-factors such as NADPH and Malonyl-CoA. Our goal is to map bacterial response to metabolic engineering aimed at producing chemical compounds sustainably.

Directed evolution of living systems allows selection for improved biomolecules, but robust, stable and reliable systems are important, and particularly targeted and multiplexed insertion into the genome.

Forward genetic screens are 'phenotype to genotype' approaches that involve modulating the expression of many genes, selecting the cells or organisms with a phenotype of interest, and then characterizing the mutations that result in those phenotypic changes. We are using this approach to map cellular responses and the adaptation to strain engineering that will enable predictive strain optimization and refactoring.